*BioSystems*, 28 (1992) 211-212
Elsevier Scientific Publishers Ireland Ltd.



# Subject Index
## Volume 28

abiotic factors, ontogenesis, variations of ontogenetic development in ostracods, biotic factors, 179
algae, endosymbiosis, plastids, bacteria, land plants, 75
algae, plastid, monophyletic, polyphyletic, evolution, 57
ambiregnal species, Codes of Nomenclature, kingdoms, protists, higher taxonomic categories, 1
ampullocysts, karyorelictid ciliates, extrusomes, nematocysts, rhabdocysts, pigment granules, 195
Archaebacteria, progenote, protein evolution, DNA polymerases, DNA topoisomerases, 15
Ascomycete evolution, Basidiomycete, fungal phylogeny, 18S ribosomal RNA gene, 117

bacteria, endosymbiosis, plastids, algae, land plants, 75
Basidiomycete, Ascomycete evolution, fungal phylogeny, 18S ribosomal RNA gene, 117
biotic factors, ontogenesis, variations of ontogenetic development in ostracods, abiotic factors, 179

central metabolism, *Giardia*, *Entamoeba*, *Trichomonas*, hydrogenosome, evolution of metabolism, 33
*Chlorarachnion reptans*, *pyrenomonas salina*, cryptophyta, nucleomorph, genomes, 69
*Chlorarachnion*, chloroplasts, mitochondria, endsymbiosis, cryptomonads, Chromista, 91
chloroplasts, mitochondria, endosymbiosis, cryptomonads, *Chlorarachnion*, Chromista, 91
Chromista, chloroplasts, mitochondria, endosymbiosis, cryptomonads, *Chlorarachnion*, 91
coccolith ultrastructure, coccolithophorid evolution, life-cycle, miocene, neogene, recent, 169
coccolithophorid evolution, life-cycle, coccolith ultrastructure, miocene, neogene, recent, 169
Codes of Nomenclature, kingdoms, protists, ambiregnal species, higher taxonomic categories, 1
compatibility analysis, lateral transfer, endosymbiosis, variant filter, 47
cryptomonads, chloroplasts, mitochondria, endosymbiosis, *Chlorarachnion*, Chromista, 91
cryptophyta, *pyrenomonas salina*, nucleomorph, genomes, *Chlorarachnion reptans*, 69
cytochrome *c* oxidase subunit III, RNA editing, trypanosomes, mitochondria, kinetoplast, molecular evolution, RNA processing and transcription, 41
cytoskeleton, morphogenesis, division, flagella, euglenoids, entosiphon, 203

division, morphogenesis, flagella, cytoskeleton, euglenoids, entosiphon, 203
DNA polymerases, progenote, protein evolution, DNA topoisomerases, Archaebacteria, 15
DNA topoisomerases, progenote, protein evolution, DNA polymerases, Archaebacteria, 15

embryophyte evolution, phylogenetic analysis, green algal evolution, origin of land plants, nuclear-encoded rRNA sequences, 127
endosymbiosis, chloroplasts, mitochondria, cryptomonads, *Chlorarachnion*, Chromista, 91
endosymbiosis, lateral transfer, compatibility analysis, variant filter, 47
endosymbiosis, plastids, bacteria, algae, land plants, 75
*Entamoeba*, *Giardia*, *Trichomonas*, central metabolism, hydrogenosome, evolution of metabolism, 33
entosiphon, morphogenesis, division, flagella, cytoskeleton, euglenoids, 203
euglenoids, morphogenesis, division, flagella, cytoskeleton, entosiphon, 203
evolution of metabolism, *Giardia*, *Entamoeba*, *Trichomonas*, central metabolism, hydrogenosome, 33
evolution, paleobiology, ostracode, pore canal, Theta-Rho, least square, 153
evolution, plastid, algae, monophyletic, polyphyletic, 57
extrusomes, karyorelictid ciliates, nematocysts, rhabdocysts, ampullocysts, pigment granules, 195

flagella, morphogenesis, division, cytoskeleton, euglenoids, entosiphon, 203
fungal phylogeny, Ascomycete evolution, Basidiomycete, 18S ribosomal RNA gene, 117

genomes, *pyrenomonas salina*, cryptophyta, nucleomorph, *Chlorarachnion reptans*, 69
*Giardia*, *Entamoeba*, *Trichomonas*, central metabolism, hydrogenosome, evolution of metabolism, 33
green algal evolution, phylogenetic analysis, origin of land plants, embryophyte evolution, nuclear-encoded rRNA sequences, 127

higher taxonomic categories, Codes of Nomenclature, kingdoms, protists, ambiregnal species, 1
hydrogenosome, *Giardia*, *Entamoeba*, *Trichomonas*, central metabolism, evolution of metabolism, 33

karyorelictid ciliates, extrusomes, nematocysts, rhabdocysts, ampullocysts, pigment granules, 195
kinetoplast, RNA editing, trypanosomes, mitochondria, cytochrome *c* oxidase subunit III, molecular evolution, RNA processing and transcription, 41
kingdoms, Codes of Nomenclature, protists, ambiregnal species, higher taxonomic categories, 1

land plants, endosymbiosis, plastids, bacteria, algae, 75
lateral transfer, endosymbiosis, compatibility analysis, variant filter, 47
least square, paleobiology, ostracode, pore canal, Theta-Rho, evolution, 153
life-cycle, coccolithophorid evolution, coccolith ultrastructure, miocene, neogene, recent, 169

metazoa, phylogeny, porifera, ribosomal RNA, 139
miocene, coccolithophorid evolution, life-cycle, coccolith ultrastructure, neogene, recent, 169
mitochondria, chloroplasts, endosymbiosis, cryptomonads, *Chlorarachnion*, Chromista, 91
mitochondria, RNA editing, trypanosomes, kinetoplast, cytochrome *c* oxidase subunit III, molecular evolution, RNA processing and transcription, 41
molecular evolution, RNA editing, trypanosomes, mitochondria, kinetoplast, cytochrome *c* oxidase subunit III, RNA processing and transcription, 41
monophyletic, plastid, algae, polyphyletic, evolution, 57
morphogenesis, division, flagella, cytoskeleton, euglenoids, entosiphon, 203

nematocysts, karyorelictid ciliates, extrusomes, rhabdocysts, ampullocysts, pigment granules, 195
neogene, coccolithophorid evolution, life-cycle, coccolith ultrastructure, miocene, recent, 169
nuclear-encoded rRNA sequences, phylogenetic analysis, green algal evolution, origin of land plants, embryophyte evolution, 127
nucleomorph, *pyrenomonas salina*, cryptophyta, genomes, *Chlorarachnion reptans*, 69

ontogenesis, variations of ontogenetic development in ostracods, biotic factors, abiotic factors, 179
origin of land plants, phylogenetic analysis, green algal evolution, embryophyte evolution, nuclear-encoded rRNA sequences, 127
ostracode, paleobiology, pore canal, Theta-Rho, least square, evolution, 153

paleobiology, ostracode, pore canal, Theta-Rho, least square, evolution, 153
Phaeophyta, Rhodophyta, ribosomal RNA, phylogeny, 109
phylogenetic analysis, green algal evolution, origin of land plants, embryophyte evolution, nuclear-encoded rRNA sequences, 127
phylogeny, metazoa, porifera, ribosomal RNA, 139
phylogeny, Phaeophyta, Rhodophyta, ribosomal RNA, 109
pigment granules, karyorelictid ciliates, extrusomes, nematocysts, rhabdocysts, ampullocysts, 195
plastid, algae, monophyletic, polyphyletic, evolution, 57
plastids, endosymbiosis, bacteria, algae, land plants, 75
polyphyletic, plastid, algae, monophyletic, evolution, 57
pore canal, paleobiology, ostracode, Theta-Rho, least square, evolution, 153
porifera, metazoa, phylogeny, ribosomal RNA, 139
progenote, protein evolution, DNA polymerases, DNA topoisomerases, Archaebacteria, 15
protein evolution, progenote, DNA polymerases, DNA topoisomerases, Archaebacteria, 15
protists, Codes of Nomenclature, kingdoms, ambiregnal species, higher taxonomic categories, 1
*Pyrenomonas salina*, cryptophyta, nucleomorph, genomes, *Chlorarachnion reptans*, 69

recent, coccolithophorid evolution, life-cycle, coccolith ultrastructure, miocene, neogene, 169
rhabdocysts, karyorelictid ciliates, extrusomes, nematocysts, ampullocysts, pigment granules, 195
Rhodophyta, Phaeophyta, ribosomal RNA, phylogeny, 109
ribosomal RNA, metazoa, phylogeny, porifera, 139
ribosomal RNA, Phaeophyta, Rhodophyta, phylogeny, 109
18S ribosomal RNA gene, Ascomycete evolution, Basidiomycete, fungal phylogeny, 117
RNA editing, trypanosomes, mitochondria, kinetoplast, cytochrome *c* oxidase subunit III, molecular evolution, RNA processing and transcription, 41
RNA processing and transcription, RNA editing, trypanosomes, mitochondria, kinetoplast, cytochrome *c* oxidase subunit III, molecular evolution, 41

Theta-Rho, paleobiology, ostracode, pore canal, least square, evolution, 153
*Trichomonas*, *Giardia*, *Entamoeba*, central metabolism, hydrogenosome, evolution of metabolism, 33
trypanosomes, RNA editing, mitochondria, kinetoplast, cytochrome *c* oxidase subunit III, molecular evolution, RNA processing and transcription, 41

variant filter, lateral transfer, endosymbiosis, compatibility analysis, 47
variations of ontogenetic development in ostracods, ontogenesis, biotic factors, abiotic factors, 179

*BioSystems*, 28 (1992) 213
Elsevier Scientific Publishers Ireland Ltd.



# Author Index

## Volume 28

Benachenhou-Lahfa, N. 15
Benson, R.H. 153
Berbee, M.L. 117
Bertholon, L. 179
Boury-Esnault, N. 139
Braccini, E. 153
Brugerolle, G. 203
Buchheim, M.A. 127

Carbonel, P. 179
Cavalier-Smith, T. 91
Chapman, R.L. 127
Christen, R. 139
Confalonieri, F. 15
Corliss, J.O. 1

Delwiche, C.F. 75
Douglas, S.E. 57
Druehl, L.D. 109
Duguet, M. 15

Elie, C. 15

Forterre, P. 15

Janin, M.-C. 169

Kraft, G. 109
Kuhsel, M. 75

Labedan, B. 15
Lafay, B. 139
Landweber, L.F. 41

Maier, U.-G. 69
Margulis, L. 107
Morden, C.W. 75
Müller, M. 33

Palmer, J.D. 75
Peypouquet, J.P. 153

Ragan, M.A. 47
Raikov, I.B. 195

Saunders, G.W. 109

Tan, I.H. 109
Taylor, J.W. 117

Vacelet, J. 139